Synchronization of epidemic oscillations induced by social network control

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Summary

Introduction

- Epidemics modeling on networks
- Oscilations induced by feedback
- Phase reconstruction
- e Results
 - Empirical data
 - Simulations
- Conclusions and perspectives

A brief introduction to epidemiology

Epidemiology is defined as the study and analysis of the distribution, determinants and control of health and diseases conditions in defined populations and been a cornerstone of public health research since the 19th century (Anderson and May, 1991; Fred and Carlos, 2001)

Epidemic models generally assume that the population can be divided into different classes or compartments depending on the stage of the disease (Anderson and May, 1992; Diekmann and Heesterbeek, 2000; Keeling and Rohani, 2007)

Simplest mathematical epidemic models \rightarrow SIS and SIR

Population divided in classes eg. SIR

$$S + I + R = 1$$

- S = Susceptible fraction
- I = Infected fraction
- R =Recovered fraction

Two processes

1 Infection (with rate β)

$$S + I \xrightarrow{\beta} I + I$$
 (2)

2 Recovery (with rate γ)

$$I \xrightarrow{\gamma} R$$

(1)

(3)

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Infection rate

$$R_0 = \beta / \gamma$$

if $R_0 > 1$ it is called endemic state.

These beyond simple models can be fitted to real data

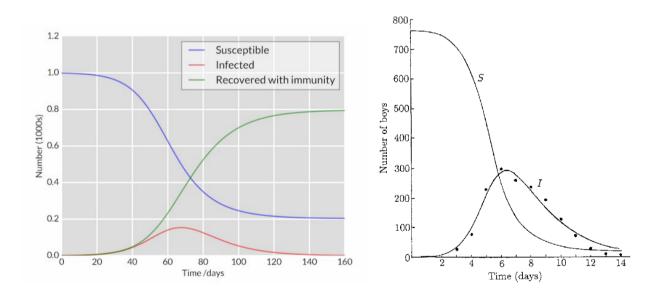


Figure 1: (Left) Stereotyped curves of the model. (Right) Fitted data for flu epidemics in a school, Murray 1989.

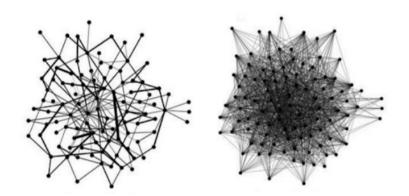
(4)

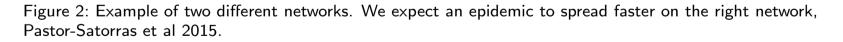
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On networks...

...the infection rate on these models also depend on the (physical) social network.

$$R_0 = \beta / \gamma \frac{\langle k^2 \rangle}{\langle k \rangle} \tag{5}$$





The key here is...

...by controlling the connectivity of the network one can also control the spreading of the infection.

Epidemic models in networks with feedback

Infection state \longleftrightarrow Network structure

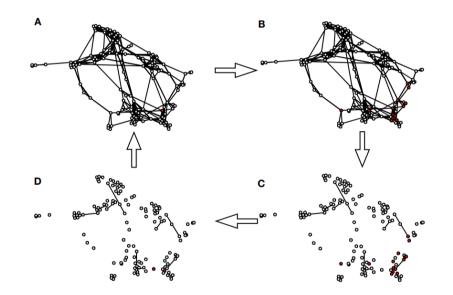


Figure 3: Example of feedback control on networks, Caccioli and De Martino 2020. A school friendship network, Mastrandrea 2015.

The idea is to simulate lockdowns.

Introduction Oscilations induced by feedback

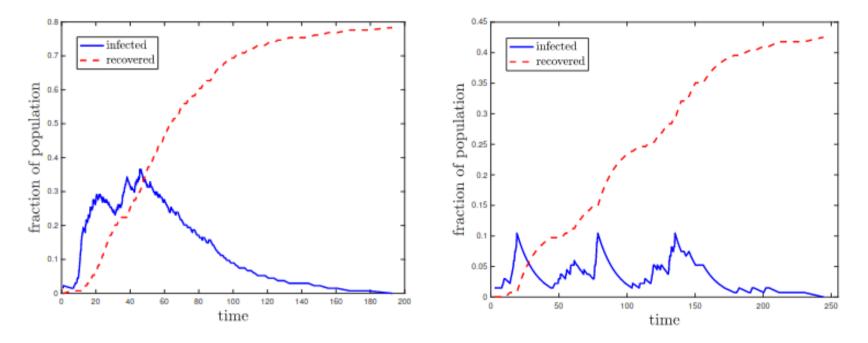


Figure 4: Feedback control impact on the SIR model. (Left) No feedback model. (Right) Feedback online. Results for a school friendship network, Mastrandrea 2015.

It is shown the emergence of a closed trajectory in real data.

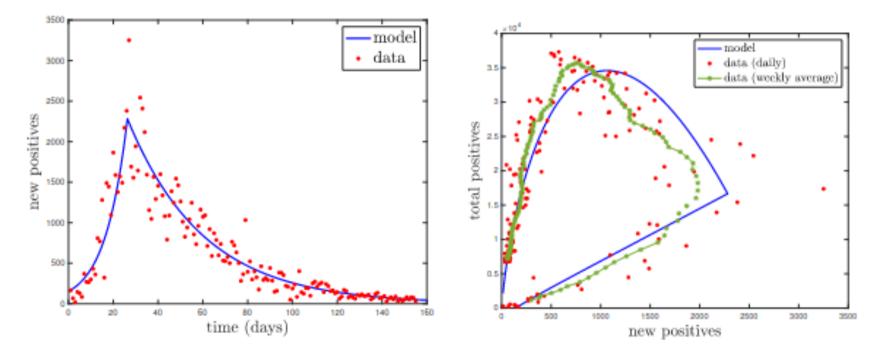


Figure 5: Data for the first epidemic wave from the region of Lombardy.

Introduction

Phase reconstruction

Now that we are treating oscillators...

Are these oscillators coupled? Is there any type of synchronization between them?

Phase reconstruction!

Hilbert transform

$$Y(t) = \hat{H}[X(t)] = \frac{1}{\pi} \int_{t_0}^{t_m} \frac{X(t')}{t - t'} dt'$$
(6)

look at data, extract the phase for each country and compare.

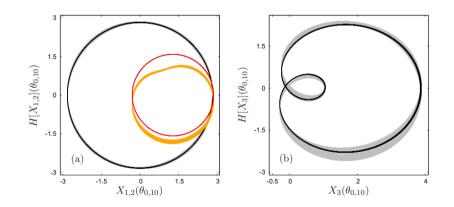


Figure 6: Example of Iterated Hilbert transform embedding for an periodically driven Stuart-Landau oscillator, Gengel and Pikovsky 2020. If trajectories are closed, the phase can tell us if different oscillators are synchronized by knowing exactly where in their own trajectory they are.

Results Empirical Data

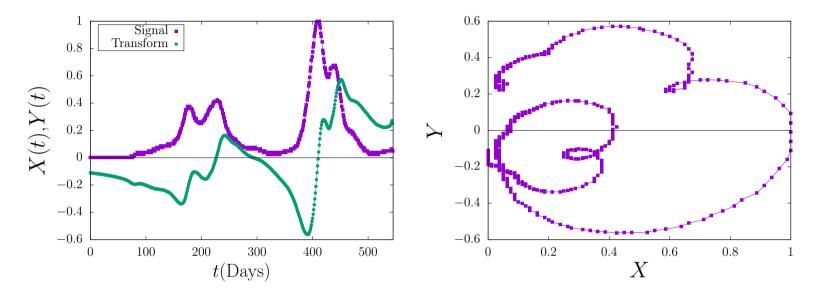
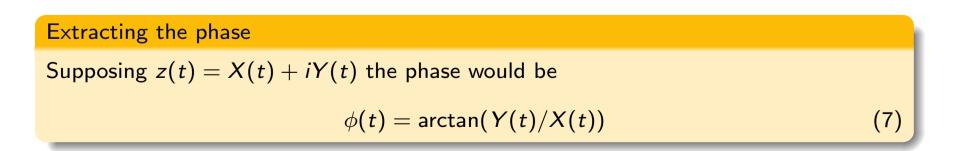


Figure 7: Example of analyzed data ¹. (Left) Signal and its Hilbert transform for Ghana as example. (Right) Phase space for the same country.



¹https://github.com/Covid19Dynamics/trajectories

Results Empirical Data

We define

$$L_{ij} = \int_{0}^{t_m} |\Delta \phi_{ij}(t)| dt = \int_{0}^{t_m} |\phi_i(t) - \phi_j(t)| dt$$
(8)

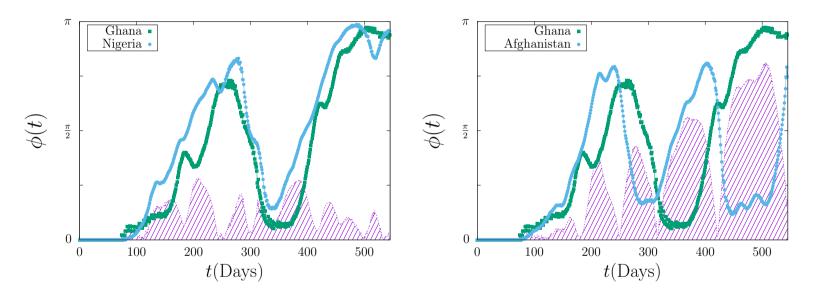


Figure 8: Integral of the modulus of the phase difference, two examples. Purple area represents the integral of the modulus of the phase difference in each case.

If we have some relation between these countries we should see some kind of block structure on the synchronization matrix L.



First attempt with 20 countries organized on regions (8 from South America, 4 from Africa and 8 for Europe).

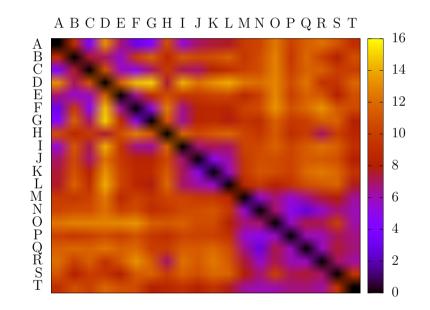


Figure 9: Block structure on the synchronization matrix *L*.

The matrix can be decomposed in blocks! Now our goal is to optimize the block structure using our migration hypothesis through some clustering algorithm.

We gathered all data available to us and followed the above discussed procedures to arrive on a 164 \times 164 synchronization matrix.

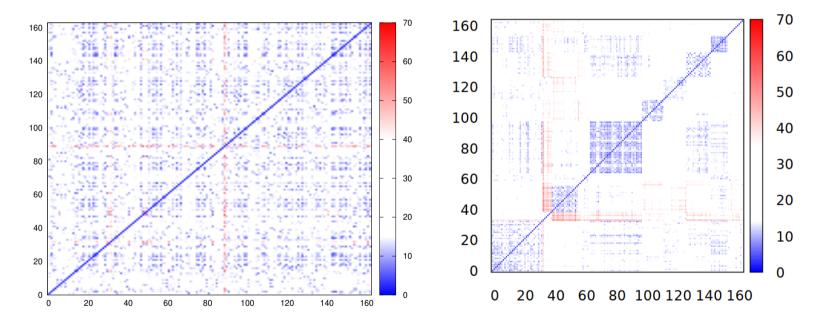


Figure 10: Worldwide synchronization matrix and (Right) our first attempt of block structure.

Now we want to explain and model these structures.

Model proposal

It is then proposed a model with migration/connectivity between two previously independent networks:

At each time a node would try to contaminate its own network it also has a (smaller) chance to infect some node of the adjacent population.

Alongside with the average connectivity of the network $\langle k \rangle_I$ we also have an average migration connectivity $\langle k \rangle_E$.

Two clear limits:

 $\langle k \rangle_E = 0 \longleftrightarrow$ Completely independent networks

 $\langle k \rangle_E = \langle k \rangle_I \longleftrightarrow$ One huge network



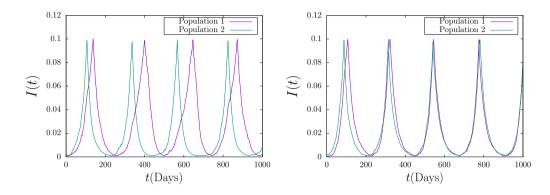


Figure 11: Impact of migration on Poissonian networks of average degree $\langle k \rangle_I = 6$ subject to feedback control. (Left) $\langle k \rangle_E = 0$. (Right) $\langle k \rangle_E = 1$.

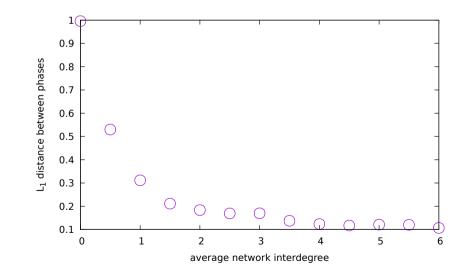


Figure 12: Distance between phases as a function of the average network interdegree $\langle k \rangle_E$.

Conclusions

- We have elaborated a synchronization matrix for the worldwide data for the Covid-19 epidemic wave.
- We also have shown that this matrix can be decomposed in a block structure.
- We propose a mechanism for this synchronization between two populations and model it.

Perspectives

- Optimize the clustering algorithm so we can in some way minimize distance between countries.
- Estimate a synchronization parameter for each group of synchronized countries (Kuramoto parameter).